WE CLAIM:

1. A substantially-purified nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of SEQ NO: 1 through SEQ NO: 580 or fragments thereof, substantial homologues thereof, and substantial complements thereof.

2. The nucleic acid molecule according to claim 1, wherein said nucleic acid molecule has a nucleic acid sequence of a fragment of one of SEQ NO: 1 through SEQ NO: 580 or a substantial homologue thereof or a substantial complement thereof and contains at least 40 nucleotides.

3. The nucleic acid molecule according to claim 2, wherein said fragment has at least 60 nucleotides.

4. The nucleic acid molecule according to claim 3, wherein said fragment has at least 100 nucleotides.

5. The nucleic acid molecule according to claim 2, wherein said fragment has a sequence that is identical or complementary to at least 50 contiguous nucleotides in one of SEQ NO: 1 through SEQ NO: 580.

6. The nucleic acid molecule according to claim 1, wherein said substantial homologues share at least 90% sequence identity with at least one of SEQ NO: 1 through SEQ NO: 580.

7. The nucleic acid molecule according to claim 6, wherein said substantial homologues share at least 95% sequence identity with at least one of SEQ NO: 1 through SEQ NO: 580.

8. The nucleic acid molecule according to claim 1, wherein said substantial homologues differ in sequence identity from at least one of SEQ NO: 1 through SEQ NO: 580 by no more than 5 nucleotides.

9. The nucleic acid molecule according to claim 8, wherein said substantial homologues differ in sequence identity from at least one of SEQ NO: 1 through SEQ NO: 580 by no more than 3 nucleotides.

10. The nucleic acid molecule according to claim 1, wherein said substantial complements share at least 90% sequence identity with at least one completely complementary sequence of SEQ NO: 1 through SEQ NO: 580.

11. The nucleic acid molecule according to claim 10, wherein said substantial complements share at least 95% sequence identity with at least one completely complementary sequence of SEQ NO: 1 through SEQ NO: 580.

12. The nucleic acid molecule according to claim 1, wherein said substantial complements differ in sequence identity from at least one completely complementary sequence of SEQ NO: 1 through SEQ NO: 580 by no more than 5 nucleotides.

13. The nucleic acid molecule according to claim 12, wherein said substantial complements differ in sequence identity from at least one completely complementary sequence of SEQ NO: 1 through SEQ NO: 580 by no more than 3 nucleotides.

14. The nucleic acid molecule according to claim 1, wherein said nucleic acid molecule shares between 95% and 100% sequence identity with at least one nucleic acid sequence selected from the group consisting of SEQ NO: 1 through SEQ NO:580 and complements thereof.

15. The nucleic acid molecule according to claim 14, wherein said nucleic acid molecule shares between 98% and 100% sequence identity with at least one nucleic acid sequence selected from the group consisting of SEQ NO: 1 through SEQ NO:580 and complements thereof.

16. The nucleic acid molecule according to claim 1, wherein said nucleic acid molecule is a carcinogenesis biomarker nucleic acid molecule selected from the group consisting of SEQ NO:1 though SEQ NO:580.

17. An amplification primer selected from the group consisting of SEQ NO: 519 though SEQ NO: 580.

18. A detection probe selected from the group consisting of SEQ NO: 490 though SEQ NO: 519.

19. A substantially-purified carcinogenesis biomarker or fragment thereof encoded by a first nucleic acid molecule which substantially hybridizes to a second nucleic acid molecule, said second nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of SEQ NO:1 through SEQ NO:580 and complements thereof.

20. The carcinogenesis biomarker or fragment thereof according to claim 19, wherein said nucleic acid sequence is a carcinogenesis biomarker encoded by a first nucleic acid molecule which substantially hybridizes to a second nucleic acid molecule, said second nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of SEQ NO:1 through SEQ NO:580 and complements thereof.

21. A substantially-purified polypeptide encoded by SEQ NO: 1 through SEQ NO: 580.

22. A method of measuring the carcinogenicity of a compound comprising:

a) exposing an animal to the compound; and

b) determining the presence or absence of a polypeptide encoded by SEQ NO:1 through SEQ NO:580.

23. A substantially-purified antibody or fragment thereof, said antibody or fragment thereof capable of specifically binding to the carcinogenesis biomarker or fragment thereof of claim 21.

24. A method of claim 22 wherein said carinogenesis measurement is determined using a substantially-purified antibody or fragment thereof, said antibody capable of specifically-binding to a substantially-purified polypeptide encoded by SEQ NO:1 through SEQ NO:580.

25. A method for determining a level or pattern of a carcinogenesis biomarker in a cell comprising:

(A) incubating, under conditions permitting nucleic acid hybridization, a marker nucleic acid molecule, said marker nucleic acid molecule having a nucleic acid sequence selected from the group consisting of SEQ NO:1 through SEQ NO:580 or complements thereof, with a complementary nucleic acid molecule obtained from said cell, wherein nucleic acid hybridization between said marker nucleic acid molecule, and said complementary nucleic acid molecule obtained from said cell permits the detection of said carcinogenesis biomarker;

(B) permitting hybridization between said marker nucleic acid molecule and said complementary nucleic acid molecule obtained from said cell; and

(C) detecting the level or pattern of said complementary nucleic acid, wherein the detection of said complementary nucleic acid is predictive of the level or pattern of said carcinogenesis biomarker.

26. The method of claim 25, wherein said level is predictive of said carcinogenesis biomarker.

27. The method of claim 25, wherein said pattern is predictive of said carcinogenesis biomarker.

28. The method of claim 25, wherein said level or pattern is detected by *in situ* hybridization.

29. A method of isolating a nucleic acid that encodes a carcinogenesis biomarker or fragment thereof comprising:

(A) incubating under conditions permitting nucleic acid hybridization, a first nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of SEQ NO:1 through SEQ NO:580 or complements thereof with a complementary second nucleic acid molecule obtained from a cell;

(B) permitting hybridization between said first nucleic acid molecule and said second nucleic acid molecule obtained from said cell; and

(C) isolating said second nucleic acid molecule.

30. A method of isolating a nucleic acid that encodes a carcinogenesis biomarker or fragment thereof comprising:

(A) incubating under conditions permitting nucleic acid hybridization, a first nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of a nucleic acid molecule encoding for a carcinogenesis biomarker or complement thereof,

with a complementary second nucleic acid molecule obtained from a cell;

(B) permitting hybridization between said first nucleic acid molecule and said second nucleic acid molecule obtained from said cell; and

(C) isolating said second nucleic acid molecule.

31. A method for measuring the carcinogenicity of a composition comprising:

(a) culturing a cell line;

(b) exposing said cell line to said composition; and

(c) determining the presence or absence of mRNA which substantially hybridizes to an at least one nucleic acid sequence selected from the group consisting of SEQ NO:1 through SEQ NO:580 and complements thereof.

32. A method for measuring the carcinogenicity of a composition comprising:

(a) exposing a cell, tissue sample, or test mammal to said composition; and

(b) determining the presence or absence of mRNA which substantially hybridizes to an at least one nucleic acid sequence selected from the group consisting of SEQ NO:1 through SEQ NO:580 and complements thereof.

33. The method of claim 32, wherein said mammal is a rat.